



SEQUENCE LISTING

<110> Murdin, Andrew

<120> CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
USES THEREOF

<130> 19721-007

<140> 09/428,122

<141> 1999-10-26

<150> 60/106,046

<151> 1998-10-28

<150> 60/132,271

<151> 1999-05-03

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<170> PatentIn Ver. 2.0

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Met Lys Ser Ser Phe

1

5

ccc aag ttt gta ttt tct aca ttt gct att ttc cct ttg tct atg att 163

Pro Lys Phe Val Phe Ser Thr Phe Ala Ile Phe Pro Leu Ser Met Ile

10

15

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gct acc gag aca gtt ttg gat tca agt gcg agt ttc gat ggg aat aaa 211

Ala Thr Glu Thr Val Leu Asp Ser Ser Ala Ser Phe Asp Gly Asn Lys

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Asn Gly Asn Phe Ser Val Arg Glu Ser Gln Glu Asp Ala Gly Thr Thr

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Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn Ile Pro Gly Thr Gly			
55	60	65	
aca gca atc aca aaa agc tgt ttt aac aac act aag ggc gat ttg act			355
Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr Lys Gly Asp Leu Thr			
70	75	80	85
ttc aca ggt aac ggg aac tct cta ttg ttc caa acg gtg gat gca ggc			403
Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln Thr Val Asp Ala Gly			
	90	95	100
act gta gca ggg gct gct gtt aac agc agc gtg gta gat aaa tct acc			451
Thr Val Ala Gly Ala Ala Val Asn Ser Ser Val Val Asp Lys Ser Thr			
	105	110	115
acg ttt ata ggg ttt tct tcg cta tct ttt att gcg tct cct gga agt			499
Thr Phe Ile Gly Phe Ser Ser Leu Ser Phe Ile Ala Ser Pro Gly Ser			
	120	125	130
tcg ata act acc ggc aaa gga gcc gtt agc tgc tct acg ggt agc ttg			547
Ser Ile Thr Thr Gly Lys Gly Ala Val Ser Cys Ser Thr Gly Ser Leu			
	135	140	145
agt ttg aca aaa aat gtc agt ttg ctc ttc agc aaa aac ttt tca acg			595
Ser Leu Thr Lys Asn Val Ser Leu Leu Phe Ser Lys Asn Phe Ser Thr			
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gat aat ggc ggt gct atc acc gca aaa act ctt tca tta aca ggc act			643
Asp Asn Gly Gly Ala Ile Thr Ala Lys Thr Leu Ser Leu Thr Gly Thr			
	170	175	180
aca atg tca gct ctg ttt tct gaa aat acc tcc tca aag aaa ggc gga			691
Thr Met Ser Ala Leu Phe Ser Glu Asn Thr Ser Ser Lys Lys Gly Gly			
	185	190	195
gcc att cag act tcc gat gcc ctt acc att act gga aac caa ggc gaa			739
Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr Gly Asn Gln Gly Glu			
	200	205	210
gtc tct ttt tct gac aat act tct tcg gat tct gga gct gca att ttt			787
Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser Gly Ala Ala Ile Phe			
	215	220	225
aca gaa gcc tcg gtg act att tct aat aat gct aaa gtt tcc ttt att			835
Thr Glu Ala Ser Val Thr Ile Ser Asn Asn Ala Lys Val Ser Phe Ile			

230	235	240	245	
gac aat aag gtc aca gga gcg agc tcc tca aca acg ggg gat atg tca				883
Asp Asn Lys Val Thr Gly Ala Ser Ser Ser Thr Thr Gly Asp Met Ser				
	250	255	260	
gga ggt gct atc tgt gct tat aaa act agt aca gat act aag gtc acc				931
Gly Gly Ala Ile Cys Ala Tyr Lys Thr Ser Thr Asp Thr Lys Val Thr				
	265	270	275	
ctc act gga aat cag atg tta ctc ttc agc aac aat aca tcg aca aca				979
Leu Thr Gly Asn Gln Met Leu Leu Phe Ser Asn Asn Thr Ser Thr Thr				
	280	285	290	
gcg gga gga gct atc tat gtg aaa aag ctc gaa ctg gct tcc gga gga				1027
Ala Gly Gly Ala Ile Tyr Val Lys Lys Leu Glu Leu Ala Ser Gly Gly				
	295	300	305	
ctt acc cta ttc agt aga aat agt gtc aat gga ggt aca gct cct aaa				1075
Leu Thr Leu Phe Ser Arg Asn Ser Val Asn Gly Gly Thr Ala Pro Lys				
	310	315	320	325
ggt gga gcc ata gct atc gaa gat agt ggg gaa ttg agt tta tcc gcc				1123
Gly Gly Ala Ile Ala Ile Glu Asp Ser Gly Glu Leu Ser Leu Ser Ala				
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gat agt ggt gac att gtc ttt tta ggg aat aca gtc act tct act act				1171
Asp Ser Gly Asp Ile Val Phe Leu Gly Asn Thr Val Thr Ser Thr Thr				
	345	350	355	
cct ggg acg aat aga agt agt atc gac tta gga acg agt gca aag atg				1219
Pro Gly Thr Asn Arg Ser Ser Ile Asp Leu Gly Thr Ser Ala Lys Met				
	360	365	370	
aca gct ttg cgt tct gct gct ggt aga gcc atc tac ttc tat gat ccc				1267
Thr Ala Leu Arg Ser Ala Ala Gly Arg Ala Ile Tyr Phe Tyr Asp Pro				
	375	380	385	
ata act aca gga tca tcc aca aca gtt aca gat gtc tta aaa gtt aat				1315
Ile Thr Thr Gly Ser Ser Thr Thr Val Thr Asp Val Leu Lys Val Asn				
	390	395	400	405
gag act ccg gca gat tct gca cta caa tat aca ggg aac atc atc ttc				1363
Glu Thr Pro Ala Asp Ser Ala Leu Gln Tyr Thr Gly Asn Ile Ile Phe				
	410	415	420	
aca gga gaa aag tta tca gag aca gag gcc gca gat tct aaa aat ctt				1411
Thr Gly Glu Lys Leu Ser Glu Thr Glu Ala Ala Asp Ser Lys Asn Leu				

425	430	435	
act tcg aag cta cta cag cct gta act ctt tca gga ggt act cta tct			1459
Thr Ser Lys Leu Leu Gln Pro Val Thr Leu Ser Gly Gly Thr Leu Ser			
440	445	450	
tta aaa cat gga gtg act ctg cag act cag gca ttc act caa cag gca			1507
Leu Lys His Gly Val Thr Leu Gln Thr Gln Ala Phe Thr Gln Gln Ala			
455	460	465	
gat tct cgt ctc gaa atg gac gta gga act act cta gaa cct gct gat			1555
Asp Ser Arg Leu Glu Met Asp Val Gly Thr Thr Leu Glu Pro Ala Asp			
470	475	480	485
act agc acc ata aac aat ttg gtc att aac atc agt tct ata gac ggt			1603
Thr Ser Thr Ile Asn Asn Leu Val Ile Asn Ile Ser Ser Ile Asp Gly			
490	495	500	
gca aag aag gca aaa ata gaa acc aaa gct acg tca aaa aat ctg act			1651
Ala Lys Lys Ala Lys Ile Glu Thr Lys Ala Thr Ser Lys Asn Leu Thr			
505	510	515	
tta tct gga acc atc act tta ttg gac ccg acg ggc acg ttt tat gaa			1699
Leu Ser Gly Thr Ile Thr Leu Leu Asp Pro Thr Gly Thr Phe Tyr Glu			
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aat cat agt tta aga aat cct cag tcc tac gac atc tta gag ctc aaa			1747
Asn His Ser Leu Arg Asn Pro Gln Ser Tyr Asp Ile Leu Glu Leu Lys			
535	540	545	
gct tct gga act gta aca agc acc gca gtg act cca gat cct ata atg			1795
Ala Ser Gly Thr Val Thr Ser Thr Ala Val Thr Pro Asp Pro Ile Met			
550	555	560	565
ggt gag aaa ttc cat tac ggc tat cag gga act tgg ggc cca att gtt			1843
Gly Glu Lys Phe His Tyr Gly Tyr Gln Gly Thr Trp Gly Pro Ile Val			
570	575	580	
tgg ggg aca ggg gct tct acg act gca acc ttc aac tgg act aaa act			1891
Trp Gly Thr Gly Ala Ser Thr Thr Ala Thr Phe Asn Trp Thr Lys Thr			
585	590	595	
ggc tat att cct aat ccc gag cgt atc ggc tct tta gtc cct aat agc			1939
Gly Tyr Ile Pro Asn Pro Glu Arg Ile Gly Ser Leu Val Pro Asn Ser			
600	605	610	
tta tgg aat gca ttt ata gat att agc tct ctc cat tat ctt atg gag			1987
Leu Trp Asn Ala Phe Ile Asp Ile Ser Ser Leu His Tyr Leu Met Glu			

615	620	625	
act gca aac gaa ggg ttg cag gga gac cgt gct ttt tgg tgt gct gga			2035
Thr Ala Asn Glu Gly Leu Gln Gly Asp Arg Ala Phe Trp Cys Ala Gly			
630	635	640	645
tta tct aac ttc ttc cat aag gat agt aca aaa aca cga cgc ggg ttt			2083
Leu Ser Asn Phe Phe His Lys Asp Ser Thr Lys Thr Arg Arg Gly Phe			
	650	655	660
cgc cat ttg agt ggc ggt tat gtc ata gga gga aac cta cat act tgt			2131
Arg His Leu Ser Gly Gly Tyr Val Ile Gly Gly Asn Leu His Thr Cys			
	665	670	675
tca gat aag att ctt agt gct gca ttt tgt cag ctc ttt gga aga gat			2179
Ser Asp Lys Ile Leu Ser Ala Ala Phe Cys Gln Leu Phe Gly Arg Asp			
	680	685	690
aga gac tac ttt gta gct aag aat caa ggt aca gtc tac gga gga act			2227
Arg Asp Tyr Phe Val Ala Lys Asn Gln Gly Thr Val Tyr Gly Gly Thr			
	695	700	705
ctc tat tac cag cac aac gaa acc tat atc tct ctt cct tgc aaa cta			2275
Leu Tyr Tyr Gln His Asn Glu Thr Tyr Ile Ser Leu Pro Cys Lys Leu			
	710	715	720
cgg cct tgt tgc ttg tct tat gtt cct aca gag att cct gtt ctc ttt			2323
Arg Pro Cys Ser Leu Ser Tyr Val Pro Thr Glu Ile Pro Val Leu Phe			
	730	735	740
tca gga aac ctt agc tac acc cat acg gat aac gat ctg aaa acc aag			2371
Ser Gly Asn Leu Ser Tyr Thr His Thr Asp Asn Asp Leu Lys Thr Lys			
	745	750	755
tat aca aca tat cct act gtt aaa gga agc tgg ggg aat gat agt ttc			2419
Tyr Thr Thr Tyr Pro Thr Val Lys Gly Ser Trp Gly Asn Asp Ser Phe			
	760	765	770
gct tta gaa ttc ggt gga aga gct ccg att tgc tta gat gaa agt gct			2467
Ala Leu Glu Phe Gly Gly Arg Ala Pro Ile Cys Leu Asp Glu Ser Ala			
	775	780	785
cta ttt gag cag tac atg ccc ttc atg aaa ttg cag ttt gtc tat gca			2515
Leu Phe Glu Gln Tyr Met Pro Phe Met Lys Leu Gln Phe Val Tyr Ala			
	790	795	800
cat cag gaa ggt ttt aaa gaa cag gga aca gaa gct cgt gaa ttt gga			2563
His Gln Glu Gly Phe Lys Glu Gln Gly Thr Glu Ala Arg Glu Phe Gly			

810	815	820	
agt agc cgt ctt gtg aat ctt gcc tta cct atc ggg atc cga ttt gat			2611
Ser Ser Arg Leu Val Asn Leu Ala Leu Pro Ile Gly Ile Arg Phe Asp			
825	830	835	
aag gaa tca gac tgc caa gat gca acg tac aat cta act ctt ggt tat			2659
Lys Glu Ser Asp Cys Gln Asp Ala Thr Tyr Asn Leu Thr Leu Gly Tyr			
840	845	850	
act gtg gat ctt gtt cgt agt aac ccc gac tgt acg aca aca ctg cga			2707
Thr Val Asp Leu Val Arg Ser Asn Pro Asp Cys Thr Thr Thr Leu Arg			
855	860	865	
att agc ggt gat tct tgg aaa acc ttc ggt acg aat ttg gca aga caa			2755
Ile Ser Gly Asp Ser Trp Lys Thr Phe Gly Thr Asn Leu Ala Arg Gln			
870	875	880	885
gct tta gtc ctt cgt gca ggg aac cat ttt tgc ttt aac tca aat ttt			2803
Ala Leu Val Leu Arg Ala Gly Asn His Phe Cys Phe Asn Ser Asn Phe			
890	895	900	
gaa gcc ttt agc caa ttt tct ttt gaa ttg cgt ggg tca tct cgc aat			2851
Glu Ala Phe Ser Gln Phe Ser Phe Glu Leu Arg Gly Ser Ser Arg Asn			
905	910	915	
tac aat gta gac tta gga gca aaa tac caa ttc taatgcgtta gctttggttaa			2904
Tyr Asn Val Asp Leu Gly Ala Lys Tyr Gln Phe			
920	925		
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35 40 45
 Asp Ala Gly Thr Thr Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn
 50 55 60
 Ile Pro Gly Thr Gly Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr
 65 70 75 80
 Lys Gly Asp Leu Thr Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln
 85 90 95
 Thr Val Asp Ala Gly Thr Val Ala Gly Ala Ala Val Asn Ser Ser Val
 100 105 110
 Val Asp Lys Ser Thr Thr Phe Ile Gly Phe Ser Ser Leu Ser Phe Ile
 115 120 125
 Ala Ser Pro Gly Ser Ser Ile Thr Thr Gly Lys Gly Ala Val Ser Cys
 130 135 140
 Ser Thr Gly Ser Leu Ser Leu Thr Lys Asn Val Ser Leu Leu Phe Ser
 145 150 155 160
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 165 170 175
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 180 185 190
 Ser Lys Lys Gly Gly Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr
 195 200 205
 Gly Asn Gln Gly Glu Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser
 210 215 220
 Gly Ala Ala Ile Phe Thr Glu Ala Ser Val Thr Ile Ser Asn Asn Ala
 225 230 235 240
 Lys Val Ser Phe Ile Asp Asn Lys Val Thr Gly Ala Ser Ser Ser Thr
 245 250 255
 Thr Gly Asp Met Ser Gly Gly Ala Ile Cys Ala Tyr Lys Thr Ser Thr
 260 265 270
 Asp Thr Lys Val Thr Leu Thr Gly Asn Gln Met Leu Leu Phe Ser Asn
 275 280 285
 Asn Thr Ser Thr Thr Ala Gly Gly Ala Ile Tyr Val Lys Lys Leu Glu

290 295 300
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 Gly Thr Ala Pro Lys Gly Gly Ala Ile Ala Ile Glu Asp Ser Gly Glu
 325 330 335
 Leu Ser Leu Ser Ala Asp Ser Gly Asp Ile Val Phe Leu Gly Asn Thr
 340 345 350
 Val Thr Ser Thr Thr Pro Gly Thr Asn Arg Ser Ser Ile Asp Leu Gly
 355 360 365
 Thr Ser Ala Lys Met Thr Ala Leu Arg Ser Ala Ala Gly Arg Ala Ile
 370 375 380
 Tyr Phe Tyr Asp Pro Ile Thr Thr Gly Ser Ser Thr Thr Val Thr Asp
 385 390 395 400
 Val Leu Lys Val Asn Glu Thr Pro Ala Asp Ser Ala Leu Gln Tyr Thr
 405 410 415
 Gly Asn Ile Ile Phe Thr Gly Glu Lys Leu Ser Glu Thr Glu Ala Ala
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 Asp Ser Lys Asn Leu Thr Ser Lys Leu Leu Gln Pro Val Thr Leu Ser
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 Gly Gly Thr Leu Ser Leu Lys His Gly Val Thr Leu Gln Thr Gln Ala
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 Ser Ser Ile Asp Gly Ala Lys Lys Ala Lys Ile Glu Thr Lys Ala Thr
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 Ser Lys Asn Leu Thr Leu Ser Gly Thr Ile Thr Leu Leu Asp Pro Thr
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 Gly Thr Phe Tyr Glu Asn His Ser Leu Arg Asn Pro Gln Ser Tyr Asp
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 Ile Leu Glu Leu Lys Ala Ser Gly Thr Val Thr Ser Thr Ala Val Thr

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 Pro Asp Pro Ile Met Gly Glu Lys Phe His Tyr Gly Tyr Gln Gly Thr
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 580 585 590
 Asn Trp Thr Lys Thr Gly Tyr Ile Pro Asn Pro Glu Arg Ile Gly Ser
 595 600 605
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 610 615 620
 His Tyr Leu Met Glu Thr Ala Asn Glu Gly Leu Gln Gly Asp Arg Ala
 625 630 635 640
 Phe Trp Cys Ala Gly Leu Ser Asn Phe Phe His Lys Asp Ser Thr Lys
 645 650 655
 Thr Arg Arg Gly Phe Arg His Leu Ser Gly Gly Tyr Val Ile Gly Gly
 660 665 670
 Asn Leu His Thr Cys Ser Asp Lys Ile Leu Ser Ala Ala Phe Cys Gln
 675 680 685
 Leu Phe Gly Arg Asp Arg Asp Tyr Phe Val Ala Lys Asn Gln Gly Thr
 690 695 700
 Val Tyr Gly Gly Thr Leu Tyr Tyr Gln His Asn Glu Thr Tyr Ile Ser
 705 710 715 720
 Leu Pro Cys Lys Leu Arg Pro Cys Ser Leu Ser Tyr Val Pro Thr Glu
 725 730 735
 Ile Pro Val Leu Phe Ser Gly Asn Leu Ser Tyr Thr His Thr Asp Asn
 740 745 750
 Asp Leu Lys Thr Lys Tyr Thr Thr Tyr Pro Thr Val Lys Gly Ser Trp
 755 760 765
 Gly Asn Asp Ser Phe Ala Leu Glu Phe Gly Gly Arg Ala Pro Ile Cys
 770 775 780
 Leu Asp Glu Ser Ala Leu Phe Glu Gln Tyr Met Pro Phe Met Lys Leu
 785 790 795 800
 Gln Phe Val Tyr Ala His Gln Glu Gly Phe Lys Glu Gln Gly Thr Glu

